

SEQUENCE LISTING



# 6.

<110> Agarwal, Poonam  
Aizenstein, Brian  
Arco, David  
Atilas, Myrta  
Burris, Deborah  
de Arruda Indig, Monika  
Law, Scott  
Mast, Andrea  
Marshall, David  
Miller, Carolyn  
Oldenberg, Mary  
Rasmussen, Eric  
Schneiders, Jennifer  
  
<120> Methods and Compositions for Detecting Target Sequences  
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Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly  
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Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
85 90 95  
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu  
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Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys  
115 120 125  
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp  
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145 150 155 160  
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Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn  
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Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu  
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Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu  
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Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe  
260 265 270  
Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
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Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
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Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp  
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 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
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 Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys  
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Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val  
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 Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val  
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 ctggcgcgcc tcgaggtccc gggctacgag gcggacgacg tcctggccag cctggccaag 420  
 aaggcggaaa aggagggtta cgaggtccgc atcctcaccg ccgacaaaga cttttaccag 480  
 cttctttccg accgcatcca cgtcctccac cccgaggggt acctcatcac cccggcctgg 540  
 ctttgggaaa agtacggcct gaggcccgac cagtggggcg actaccgggc cctgaccggg 600  
 gacgagtccg acaaccttcc cggggtcaag ggcacgggg agaagacggc gaggaagctt 660  
 ctggaggagt gggggagcct ggaagccctc ctcaagaacc tggaccggct gaagcccgcc 720  
 atccgggaga agatcctggc ccacatggac gatctgaagc tctcctggga cctggccaag 780  
 gtgcgcaccg acctgcccct ggaggtggac ttcgccaaaa ggcgggagcc cgaccgggag 840  
 aggcttaggg cctttctgga gaggtttgag tttggcagcc tcctccacga gttcggcctt 900  
 ctggaaagcc ccaaggccgc actcgagcac caccaccacc accactga 948

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 <211> 206  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
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<400> 27  
 cgccagggtt ttcccagtca cgacgttgta aaacgacggc cagtgaattg taatacgact 60  
 cactataggg cgaattcgag ctcggtaccc ggggatcctc tagagtcgac ctgcaggcat 120  
 gcaagcttga gtattctata gtgtcaccta aatagcttgg cgtaatcatg gtcatagctg 180  
 tttcctgtgt gaaattgtta tccgct 206  
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 <223> Synthetic  
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 aacagctatg accatgatta c 21  
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 <211> 60  
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 <220>  
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 <400> 29  
 gttctctgct ctctggtcgc tgtctcgctt gtgaaacaag cgagacagcg tggctctctcg 60  
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 <211> 15  
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 <400> 30  
 cgagagacca cgctg 15  
 <210> 31  
 <211> 52  
 <212> DNA

<213> Artificial Sequence  
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 <400> 31  
 cctttcgctt tcttccttc ctttctcgcc acgttcgcg gctttccccg tc 52  
 <210> 32  
 <211> 26  
 <212> DNA  
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 <220>  
 <223> Synthetic  
 <400> 32  
 agaaaggaag ggaagaaagc gaaagg 26  
 <210> 33  
 <211> 21  
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 <220>  
 <223> Synthetic  
 <400> 33  
 gacggggaaa gccggcgaac g 21  
 <210> 34  
 <211> 20  
 <212> DNA  
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 <223> Synthetic  
 <400> 34  
 gaaagccggc gaacgtggcg 20  
 <210> 35  
 <211> 21  
 <212> DNA

<213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 35  
 ggcgaacgtg gcgagaaagg a 21  
 <210> 36  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 36  
 cctttcgctt tcttccttc ctttctcgcc acgttcgccg gc 42  
 <210> 37  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 37  
 cctttcgctc tcttccttc ctttctcgcc acgttcgccg gc 42  
 <210> 38  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (8)..(8)  
 <223> The residue at this position is 2'-O-methyladenosine.  
 <400> 38  
 agaaaggaag ggaagaaagc gaaaggt 27



<210>	39	
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<212>	DNA	
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	gccggcggaac gtggcgagaa agga	24
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<212>	DNA	
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	ggtttttctt tgaggtttag	20
<210>	41	
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<400>	41	
	gcgacactcc accatagat	19
<210>	42	
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<212>	DNA	
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<223>	Synthetic	
<400>	42	
	ctgtcttcac gcagaaagc	19

<210> 43  
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 <212> DNA  
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 <220>  
 <223> Synthetic  
 <400> 43  
 gcacggtcta cgagacctc 19  
 <210> 44  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 44  
 taatacgact cactataggg 20  
 <210> 45  
 <211> 337  
 <212> RNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
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 gggaaagcuu gcaugccugc aggucgacuc uagaggaucau acuagucuaa uggauucugu 60  
 cuucacgcag aaagcgucug gccauggcgu uaguaugagu gucgugcagc cuccaggacc 120  
 cccccucccg ggagaggcau aguggucugc ggaaccggug aguacaccgg aaaugccagg 180  
 acgaccgggu ccuuucuugg auaaaccgcg ucaaugccug gagauuuggg cgugcccccg 240  
 caagacugcu agccgaguag uguugggucg cgaaaggccu ugugguacug ccugauaggg 300  
 ugccugcgag ugccccggga ggucucguag accgugc 337  
 <210> 46  
 <211> 19  
 <212> DNA

<213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (17)..(17)  
 <223> The T at this position is linked to a fluorescein dye on an abasic linker  
 <400> 46  
 ccggtcgtcc tggcaatcc 19  
 <210> 47  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 47  
 gtttatccaa gaaaggaccc ggtc 24  
 <210> 48  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 48  
 cagggtgaag ggaagaagaa agcgaaaggt 30  
 <210> 49  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 49  
 cagggggaag ggaagaagaa agcgaaaggt 30

<210> 50  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (1)..(2)  
 <223> The T residues at these positions are amino modified T residues.  
 <400> 50  
 ttcttttcac cagcgagacg gg 22  
 <210> 51  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
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 attgggcgcc aggggtggttt tt 22  
 <210> 52  
 <211> 53  
 <212> DNA  
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 <223> Synthetic  
 <400> 52  
 cccgtctcgc tgggtgaaaag aaaaaccacc ctggcgccca atacgcaaac cgc 53

<210>	53	
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<223>	Synthetic	
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	gaattcgatt taggtgacac tatagaatac a	31
<210>	54	
<211>	42	
<212>	DNA	
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<223>	Synthetic	
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	cctttcgctt tcttcccttc ctttctcgcc acgttcgccg gc	42
<210>	55	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
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	gccggcgaac gtggcgagaa agga	24
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<212>	DNA	
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	cagaaggaag ggaagaaagc gaaagg	26

<210>	57	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	57	
	caagggggaag ggaagaaagc gaaagg	26
<210>	58	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	58	
	caggggtacag ggaagaaagc gaaagg	26
<210>	59	
<211>	42	
<212>	DNA	
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	gggaaagtcc tcggagccgc gcgggacgag cgtggggggcc cg	42
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<220>		

<221> CDS

<222> (1) .. (960)

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atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc ctg gtg gac ggc	96
Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly	
20 25 30	
cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag ggc ctc acc acc	144
His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr	
35 40 45	
agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc gcc aag agc ctc	192
Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu	
50 55 60	
ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc gtg gtc ttt gac	240
Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp	
65 70 75 80	
gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg ggg tac aag gcg	288
Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala	
85 90 95	
ggc cgg gcc ccc acg ctc gtc ccg cgc ggc tcc gag gac ttt ccc cgg	336
Gly Arg Ala Pro Thr Leu Val Pro Arg Gly Ser Glu Asp Phe Pro Arg	
100 105 110	
caa ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc	384
Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg	
115 120 125	
ctc gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc	432
Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala	
130 135 140	
aag aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac	480
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp	
145 150 155 160	
aaa gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc	528
Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro	
165 170 175	
gag ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg	576
Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu	
180 185 190	
agg ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc	624
Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser	
195 200 205	
gac aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag	672
Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys	
210 215 220	

ctt	ctg	gag	gag	tgg	ggg	agc	ctg	gaa	gcc	ctc	ctc	aag	aac	ctg	gac	720
Leu	Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	
225					230					235					240	
cgg	ctg	aag	ccc	gcc	atc	cgg	gag	aag	atc	ctg	gcc	cac	atg	gac	gat	768
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	
				245					250					255		
ctg	aag	ctc	tcc	tgg	gac	ctg	gcc	aag	gtg	cgc	acc	gac	ctg	ccc	ctg	816
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	
			260					265					270			
gag	gtg	gac	ttc	gcc	aaa	agg	cgg	gag	ccc	gac	cgg	gag	agg	ctt	agg	864
Glu	Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	
		275					280					285				
gcc	ttt	ctg	gag	agg	ctt	gag	ttt	ggc	agc	ctc	ctc	cac	gag	ttc	ggc	912
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	
	290				295						300					
ctt	ctg	gaa	agc	ccc	aag	gcc	gca	ctc	gag	cac	cac	cac	cac	cac	cac	960
Leu	Leu	Glu	Ser	Pro	Lys	Ala	Ala	Leu	Glu	His	His	His	His	His	His	
305					310					315					320	
tga																963

<210> 61

<211> 320

<212> PRT

<213> Artificial Sequence

<400> 61

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Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	Asp	Gly
			20					25					30		

His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu	Thr	Thr
		35					40					45			

Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	Ser	Leu
	50					55					60				

Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val	Val	Phe	Asp
65					70					75					80

Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr	Lys	Ala
				85					90					95	



Gly Arg Ala Pro Thr Leu Val Pro Arg Gly Ser Glu Asp Phe Pro Arg  
                   100                  105                  110

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg  
           115                  120                  125

Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala  
       130                  135                  140

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp  
 145                  150                  155                  160

Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro  
                   165                  170                  175

Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu  
           180                  185                  190

Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser  
           195                  200                  205

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys  
       210                  215                  220

Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp  
 225                  230                  235                  240

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
                   245                  250                  255

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
           260                  265                  270

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg  
       275                  280                  285

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
       290                  295                  300

Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His His  
 305                  310                  315                  320

<210> 62

<211> 20

<212> DNA

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<221> CDS

<222> (1) .. (2499)

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ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag	96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys	
20 25 30	
ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc	144
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe	
35 40 45	
gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc	192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile	
50 55 60	
gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg	240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly	
65 70 75 80	
ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa	288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln	
85 90 95	
ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc	336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu	
100 105 110	
gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag	384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys	
115 120 125	
aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa	432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys	
130 135 140	
gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag	480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu	
145 150 155 160	
ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg	528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg	
165 170 175	
ccc gac cag tgg gcc gac tac ccg gcc ctg acc ggg gac gag tcc gac	576
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp	
180 185 190	
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt	624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu	
195 200 205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg	672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg	
210 215 220	

ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg	720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu	
225 230 235 240	
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag	768
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu	
245 250 255	
gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc	816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala	
260 265 270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt	864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu	
275 280 285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa	912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	
290 295 300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc	960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala	
305 310 315 320	
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc	1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala	
325 330 335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt	1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu	
340 345 350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc	1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu	
355 360 365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc	1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser	
370 375 380	
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg	1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr	
385 390 395 400	
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac	1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn	
405 410 415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg	1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg	
420 425 430	
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg	1344
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr	
435 440 445	
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg	1392
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val	
450 455 460	

gcc gag gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly 465 470 475 480	1440
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 490 495	1488
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys 500 505 510	1536
cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 520 525	1584
atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser 530 535 540	1632
acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg 545 550 555 560	1680
ctc cac acc cgc ttc aac cag acg gcc acg gcc acg ggc agg cta agt Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser 565 570 575	1728
agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly 580 585 590	1776
cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val 595 600 605	1824
gcc ctg gac tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser 610 615 620	1872
ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His 625 630 635 640	1920
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 645 650 655	1968
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr 660 665 670	2016
ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu 675 680 685	2064
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val 690 695 700	2112

cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac	2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr	
705 710 715 720	
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc	2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala	
725 730 735	
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg	2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	
740 745 750	
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag	2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	
755 760 765	
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc	2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val	
770 775 780	
cac aac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg	2400
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val	
785 790 795 800	
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg	2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val	
805 810 815	
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag	2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys	
820 825 830	
gag tgatag	2505
Glu	

<210> 66

<211> 833

<212> PRT

<213> Artificial Sequence

<400> 66

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235	240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	245	250	255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	260	265	270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285	
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	290	295	300	
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	305	310	315	320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560



Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu

<210> 67

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 67

tggctatagr ccagggccac

20

<210> 68

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1) .. (2499)

<400> 68

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Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

48

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

96

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

144

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

192

gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly 65 70 75 80	240
ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln 85 90 95	288
ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu 100 105 110	336
gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys 115 120 125	384
aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys 130 135 140	432
gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag Asp Leu Tyr Gln Leu Ser Asp Arg Ile His Val Leu His Pro Glu 145 150 155 160	480
ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg 165 170 175	528
ccc gac cag tgg gcc gac tac ccg gcc ctg acc ggg gac gag tcc gac Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp 180 185 190	576
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu 195 200 205	624
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg 210 215 220	672
ctg aag ccc gcc atc ccg gag aag atc ctg gcc cac atg gac gat ctg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu 225 230 235 240	720
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu 245 250 255	768
gtg gac ttc gcc aaa agg ccg gag ccc gac ccg gag agg ctt agg gcc Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala 260 265 270	816
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu 275 280 285	864
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu 290 295 300	912

ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala 305 310 315 320	960
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc Asp Leu Leu Ala Leu Ala Ala Arg Gly Arg Val His Arg Ala 325 330 335	1008
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu 340 345 350	1056
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu 355 360 365	1104
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser 370 375 380	1152
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr 385 390 395 400	1200
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn 405 410 415	1248
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg 420 425 430	1296
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr 435 440 445	1344
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val 450 455 460	1392
gcc ggg gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly 465 470 475 480	1440
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 490 495	1488
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys 500 505 510	1536
cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 520 525	1584

atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser 530 535 540	1632
acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg 545 550 555 560	1680
ctc cac acc cgc ttc aac cag acg gcc acg gcc acg ggc agg cta agt Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser 565 570 575	1728
agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly 580 585 590	1776
cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val 595 600 605	1824
gcc ctg gcc tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc Ala Leu Ala Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser 610 615 620	1872
ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His 625 630 635 640	1920
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 645 650 655	1968
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr 660 665 670	2016
ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu 675 680 685	2064
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val 690 695 700	2112
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr 705 710 715 720	2160
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala 725 730 735	2208
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met 740 745 750	2256
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys 755 760 765	2304

ctc	ttc	ccc	agg	ctg	gag	gaa	atg	ggg	gcc	agg	atg	ctc	ctt	cag	gtc	2352
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	
	770					775					780					

cac	gac	gag	ctg	gtc	ctc	gag	gcc	cca	aaa	gag	agg	gcg	gag	gcc	gtg	2400
His	Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	
	785				790					795					800	

gcc	cgg	ctg	gcc	aag	gag	gtc	atg	gag	ggg	gtg	tat	ccc	ctg	gcc	gtg	2448
Ala	Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	
				805					810					815		

ccc	ctg	gag	gtg	gag	gtg	ggg	ata	ggg	gag	gac	tgg	ctc	tcc	gcc	aag	2496
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	
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gag	tgatag															2505
Glu																

<210> 69

<211> 833

<212> PRT

<213> Artificial Sequence

<400> 69

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			20					25					30		

Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			

Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				

Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80

Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	

Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		

Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Ala Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620



Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
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 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu

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ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag      96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
          20          25          30

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc      144
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
          35          40          45

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc      192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
          50          55          60

gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg      240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65          70          75          80

ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa      288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
          85          90          95

ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc      336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
          100          105          110

gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag      384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
          115          120          125

aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa      432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
          130          135          140

gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag      480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145          150          155          160

ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg      528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
          165          170          175

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ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc gac	576
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp	
180 185 190	
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt	624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu	
195 200 205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg	672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg	
210 215 220	
ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg	720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu	
225 230 235 240	
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag	768
Lys Leu Ser Trp Asp Leu Ala Lys Val Thr Asp Leu Pro Leu Glu	
245 250 255	
gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc	816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala	
260 265 270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt	864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu	
275 280 285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa	912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	
290 295 300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc	960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala	
305 310 315 320	
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc	1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala	
325 330 335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt	1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu	
340 345 350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc	1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu	
355 360 365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc	1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser	
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aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg	1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr	
385 390 395 400	
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac	1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn	
405 410 415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg	1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg	

420								425				430								
gag	gtg	gag	agg	ccc	ctt	tcc	gct	gtc	ctg	gcc	cac	atg	gag	gcc	acg	1344				
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr					
		435					440					445								
ggg	gtg	cgc	ctg	gac	gtg	gcc	tat	ctc	agg	gcc	ttg	tcc	ctg	gag	gtg	1392				
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val					
	450					455					460									
gcc	ggg	gag	atc	gcc	cgc	ctc	gag	gcc	gag	gtc	ttc	cgc	ctg	gcc	ggc	1440				
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly					
465					470					475					480					
cac	ccc	ttc	aac	ctc	aac	tcc	cgg	gac	cag	ctg	gaa	agg	gtc	ctc	ttt	1488				
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe					
			485						490					495						
gac	gag	cta	ggg	ctt	ccc	gcc	atc	ggc	aag	acg	gag	aag	acc	ggc	aag	1536				
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys					
			500					505					510							
cgc	tcc	acc	agc	gcc	gcc	gtc	ctg	gag	gcc	ctc	cgc	gag	gcc	cac	ccc	1584				
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro					
		515				520						525								
atc	gtg	gag	aag	atc	ctg	cag	tac	cgg	gag	ctc	acc	aag	ctg	aag	agc	1632				
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser					
	530					535					540									
acc	tac	att	gac	ccc	ttg	ccg	gac	ctc	atc	cac	ccc	agg	acg	ggc	cgc	1680				
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg					
545					550					555					560					
ctc	cac	acc	cgc	ttc	aac	cag	acg	gcc	acg	gcc	acg	ggc	agg	cta	agt	1728				
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser					
				565					570					575						
agc	tcc	gat	ccc	aac	ctc	cag	aac	atc	ccc	gtc	cgc	acc	ccg	ctt	ggg	1776				
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly					
			580					585					590							
cag	agg	atc	cgc	cgg	gcc	ttc	atc	gcc	gag	gag	ggg	tgg	cta	ttg	gtg	1824				
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val					
		595				600						605								
gcc	ctg	gtc	tat	agc	cag	ata	gag	ctc	agg	gtg	ctg	gcc	cac	ctc	tcc	1872				
Ala	Leu	Val	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser					
	610					615					620									
ggc	gac	gag	aac	ctg	atc	cgg	gtc	ttc	cag	gag	ggg	cgg	gac	atc	cac	1920				
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His					
625					630					635					640					
acg	gag	acc	gcc	agc	tgg	atg	ttc	ggc	gtc	ccc	cgg	gag	gcc	gtg	gac	1968				
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp					
			645					650						655						
ccc	ctg	atg	cgc	cgg	gcg	gcc	aag	acc	atc	aac	ttc	ggg	gtc	ctc	tac	2016				
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr					
			660					665					670							

ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag	2064
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu	
675 680 685	
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg	2112
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val	
690 695 700	
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac	2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr	
705 710 715 720	
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc	2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala	
725 730 735	
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg	2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	
740 745 750	
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag	2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	
755 760 765	
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc	2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val	
770 775 780	
cac gac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg	2400
His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val	
785 790 795 800	
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg	2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val	
805 810 815	
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag	2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys	
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gag tgatag	2505
Glu	

<210> 71

<211> 833

<212> PRT

<213> Artificial Sequence

<400> 71

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Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
                   35                                  40  45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
           50                                  55                                  60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
   65                                  70                                  75                                  80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
                                   85                                  90                                  95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
                                   100                                  105                                  110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
                   115                                  120                                  125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
   130                                  135                                  140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
  145                                  150                                  155                                  160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
                                   165                                  170                                  175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
                                   180                                  185                                  190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
           195                                  200                                  205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
   210                                  215                                  220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
  225                                  230                                  235                                  240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
                                   245                                  250                                  255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
                   260                                  265                                  270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
   275                                  280                                  285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605

Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780



His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
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Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830

Glu

<210> 72

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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25

<210> 73

<211> 27

<212> DNA

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<220>

<223> Synthetic

<400> 73  
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<210> 74

<211> 981

<212> DNA

<213> Artificial Sequence

<220>

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<220>

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<222> (1) .. (978)

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gaa gat tta aaa ggg aaa aaa gta gct att gat gga atg aat gca tta	96
Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu	
20 25 30	
tat cag ttt tta aca tct ata cgt ttg aga gat ggt tct cca ttg aga	144
Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg	
35 40 45	
aat aga aaa gga gag ata acc tca gca tat aac gga gtt ttt tat aaa	192
Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys	
50 55 60	
acc ata cat ttg tta gag aat gat ata act cca atc tgg gtt ttt gat	240
Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp	
65 70 75 80	
ggt gag cca cca aag tta aag gag aaa aca agg aaa gtt agg aga gag	288
Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu	
85 90 95	
atg aaa gag aaa gct gaa ctt aag atg aaa gag gca att aaa aag gag	336
Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu	
100 105 110	
gat ttt gaa gaa gct gct aag tat gca aag agg gtt agc tat cta act	384
Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr	
115 120 125	
ccg aaa atg gtt gaa aac tgc aaa tat ttg tta agt ttg atg ggc att	432
Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile	
130 135 140	
ccg tat gtt gaa gct ccc tct gag gga gag gca caa gca agc tat atg	480
Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met	
145 150 155 160	
gca aag aag gga gat gtt tgg gca gtt gta agt caa gat tat gat gcc	528
Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala	
165 170 175	
ttg tta tat gga gct ccg aga gtt gtt aga aat tta aca act aca aag	576
Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys	
180 185 190	
gag atg cca gaa ctt att gaa tta aat gag gtt tta gag gat tta aga	624
Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg	
195 200 205	
att tct ttg gat gat ttg ata gat ata gcc ata ttt atg gga act gac	672
Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp	
210 215 220	

tat aat cca gga gga gtt aaa gga ata gga ttt aaa agg gct tat gaa	720
Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu	
225 230 235 240	
ttg gtt aga agt ggt gta gct aag gat gtt ttg aaa aaa gag gtt gaa	768
Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu	
245 250 255	
tac tac gat gag att aag agg ata ttt aaa gag cca aag gtt acc gat	816
Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp	
260 265 270	
aac tat tca tta agc cta aaa ttg cca gat aaa gag gga att ata aaa	864
Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys	
275 280 285	
ttc tta gtt gat gaa aat gac ttt aat tat gat agg gtt aaa aag cat	912
Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His	
290 295 300	
gtt gat aaa ctc tat aac tta att gca aac aaa act aag caa aaa aca	960
Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr	
305 310 315 320	
tta gat gca tgg ttt aaa taa	981
Leu Asp Ala Trp Phe Lys	
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<210> 75

<211> 326

<212> PRT

<213> Artificial Sequence

<400> 75

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Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
35 40 45

Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
50 55 60

Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
85 90 95

Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu  
 100 105 110

Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr  
 115 120 125

Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile  
 130 135 140

Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met  
 145 150 155 160

Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala  
 165 170 175

Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys  
 180 185 190

Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg  
 195 200 205

Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp  
 210 215 220

Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu  
 225 230 235 240

Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu  
 245 250 255

Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp  
 260 265 270

Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys  
 275 280 285

Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His  
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Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr  
 305 310 315 320

Leu Asp Ala Trp Phe Lys  
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<210> 76  
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 <212> DNA  
 <213> Artificial Sequence  
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 <400> 76  
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 <212> DNA  
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 <400> 77  
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 <212> DNA  
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 1 5 10 15  
 gaa aac cta tac ggg aaa aaa atc gca atc gac gct ctt aat gca atc 96  
 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile  
 20 25 30  
 tac caa ttt ttg tcc aca ata aga cag aaa gat gga act cca ctt atg 144  
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met  
 35 40 45

gat tca aag ggt aga ata acc tcc cac cta agc ggg ctc ttt tac agg Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg 50 55 60	192
aca ata aac cta atg gag gct gga ata aaa cct gtg tat gtt ttt gat Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp 65 70 75 80	240
gga gaa cct cca gaa ttc aaa aag aaa gag ctc gaa aaa aga aga gaa Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu 85 90 95	288
gcg aga gag gaa gct gaa gaa aag tgg aga gaa gca ctt gaa aaa gga Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly 100 105 110	336
gag ata gag gaa gca aga aaa tat gcc caa aga gca acc agg gta aat Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn 115 120 125	384
gaa atg ctc atc gag gat gca aaa aaa ctc tta gag ctt atg gga att Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile 130 135 140	432
cct ata gtt caa gca cct agc gag gga gag gcc caa gct gca tat atg Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met 145 150 155 160	480
gcc gca aag ggg agc gtg tat gca tcg gct agt caa gat tac gat tcc Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser 165 170 175	528
cta ctt ttt gga gct cca aga ctt gtt aga aac tta aca ata aca gga Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly 180 185 190	576
aaa aga aag ttg cct ggg aaa aat gtc tac gtc gag ata aag ccc gag Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu 195 200 205	624
ttg ata att ttg gag gaa gta ctc aag gaa tta aag cta aca aga gaa Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu 210 215 220	672
aag ctc att gaa cta gca atc ctc gtt gga aca gac tac aac cca gga Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly 225 230 235 240	720
gga ata aag ggc ata ggc ctt aaa aaa gct tta gag att gtt aga cac Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His 245 250 255	768
tca aaa gat ccg cta gca aag ttc caa aag caa agc gat gtg gat tta Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu 260 265 270	816
tat gca ata aaa gag ttc ttc cta aac cca cca gtc aca gat aac tac Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr 275 280 285	864

aat tta gtg tgg aga gat ccc gac gaa gag gga ata cta aag ttc tta	912
Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu	
290 295 300	
tgt gac gag cat gac ttt agt gag gaa aga gta aag aat gga tta gag	960
Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu	
305 310 315 320	
agg ctt aag aag gca atc aaa agt gga aaa caa tca acc ctt gaa agt	1008
Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser	
325 330 335	
tgg ttc aag aga taa	1023
Trp Phe Lys Arg	
340	
<210> 79	
<211> 340	
<212> PRT	
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Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu	
1 5 10 15	
Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile	
20 25 30	
Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met	
35 40 45	
Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg	
50 55 60	
Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp	
65 70 75 80	
Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu	
85 90 95	
Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly	
100 105 110	
Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn	
115 120 125	
Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile	
130 135 140	

Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met  
 145 150 155 160  
 Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser  
 165 170 175  
 Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly  
 180 185 190  
 Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu  
 195 200 205  
 Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu  
 210 215 220  
 Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly  
 225 230 235 240  
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His  
 245 250 255  
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu  
 260 265 270  
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr  
 275 280 285  
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu  
 290 295 300  
 Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu  
 305 310 315 320  
 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser  
 325 330 335  
 Trp Phe Lys Arg  
 340

<210> 80

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic



<400> 80  
 gataccatgg gtgtcccaat tgggtg 25  
 <210> 81  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 81  
 tcgacgtcga cttatctctt gaaccaactt tcaaggg 37  
 <210> 82  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 82  
 agcgagggag aggcccaagc 20  
 <210> 83  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 83  
 gcctatgccc tttattcctc c 21  
 <210> 84  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 84  
 tggtcgctgt ctcgctgaaa gcgagacagc gtg 33

<210> 85  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 85  
 tgctctctgg tcgctgtctg aaagacagcg 30  
 <210> 86  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> The residue at this position is linked to a spacer containing a f  
 luorescein label  
 <400> 86  
 agaaaggaag ggaagaaagc gaaagg 26  
 <210> 87  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (26)..(26)  
 <223> The residue at this position is linked to a spacer bearing a Cy3  
 dye

<220>  
 <221> modified\_base  
 <222> (27)..(27)  
 <223> The residue at this position is a dideoxycytidine.  
 <400> 87  
 agaaaggaag ggaagaaagc gaaaggc 27  
 <210> 88  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (24)..(24)  
 <223> The residue at this position is a dideoxycytidine.  
 <400> 88  
 gccggcggaac gtggcgagaa aggc 24  
 <210> 89  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> The residue at this position is linked to a spacer containing a f  
 luorescein label

<220>  
 <221> misc\_feature  
 <222> (26)..(26)  
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye  
 <220>  
 <221> modified\_base  
 <222> (27)..(27)  
 <223> The residue at this position is a dideoxycytidine.  
 <400> 89  
 agaaaggaag ggaagaaagc gaaaggc 27  
 <210> 90  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 90  
 aaaattcctt tctctttgcc ctttgcttcc 30  
 <210> 91  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 91  
 ggaaagccgg cgaacgtggc gagaaa 26  
 <210> 92  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic

<400> 92  
 ggaaagccgg cgaacgtggc gaga 24  
 <210> 93  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> The residue at this position is linked to a spacer containing Cy3  
 <220>  
 <221> misc\_feature  
 <222> (26)..(26)  
 <223> The residue at this position is linked to a spacer containing a f  
 luorescein label  
 <400> 93  
 agaaaggaag ggaagaaagc gaaaggt 27  
 <210> 94  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> The residue at this position is linked to a spacer containing Cy3

<220>  
 <221> modified\_base  
 <222> (1)..(2)  
 <223> The residues at these positions are amine-T.  
 <220>  
 <221> misc\_feature  
 <222> (22)..(22)  
 <223> The residue at this position is linked to a spacer containing a f  
 luorescein label  
 <400> 94  
 ttccagagcc taatttgcca gta 23  
 <210> 95  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (1)..(1)  
 <223> The residue at this position has a 5' TET-label.  
 <220>  
 <221> misc\_feature  
 <222> (22)..(22)  
 <400> 95  
 ttccagagcc taatttgcca gta 23  
 <210> 96  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic

<400> 96  
 cttaccaacg ctaacgagcg tcttg 25  
 <210> 97  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 97  
 cccgtctcgc tggtgaaaag aaaaaccacc ctggcgccca ata 43  
 <210> 98  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 98  
 tattgggcgc catggtggtt ttt 23  
 <210> 99  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (10)..(10)  
 <223> The residue at this position is a 5-nitroindole.  
 <220>  
 <221> misc\_difference  
 <222> (16)..(16)  
 <223> The residue at this position is a 5-nitroindole.

<400> 99  
 tattgggcn cagggnggtt ttt 23  
  
 <210> 100  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (10)..(10)  
 <223> The residue at this position is a 5-nitroindole.  
 <220>  
 <221> misc\_difference  
 <222> (16)..(16)  
 <223> The residue at this position is a 5-nitroindole.  
  
 <400> 100  
 tattgggcn catggnggtt ttt 23  
  
 <210> 101  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (16)..(16)  
 <223> The residue at this position is a 3-nitropyrrole group.  
  
 <400> 101  
 tattgggcn cagggnggtt ttt 23



<210> 102  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (16)..(16)  
 <223> The residue at this position is a 3-nitropyrrole group.  
 <400> 102  
 tattgggcgc catggngggtt ttt 23  
 <210> 103  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (1)..(1)  
 <223> The residue at this position is a 2'deoxyctosine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (2)..(2)  
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (3)..(3)  
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo  
 nophosphate)

<220>  
 <221> misc\_difference  
 <222> (4)..(5)  
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (6)..(6)  
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (7)..(7)  
 <223> The residue at this position is a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (8)..(8)  
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (9)..(10)  
 <223> The residue at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)  
 <400> 103  
 ctgaatataa acttggtgga gttggagctg gtgccgtagg caagagtgcc ttgacg 56  
 <210> 104  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic

<220>  
 <221> misc\_difference  
 <222> (1)..(1)  
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (2)..(2)  
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (3)..(3)  
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (4)..(5)  
 <223> The residue at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (6)..(6)  
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (7)..(7)  
 <223> The residue at this position is a 2'deoxyadenosine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (8)..(8)  
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo  
 nophosphate)

<220>

<221> misc\_difference

<222> (9)..(10)

<223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)

<400> 104  
ctgaatataa acttgtggta gttggagctg gtgacgtagg caagagtgcc ttgacg 56

<210> 105

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc\_difference

<222> (1)..(1)

<223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc\_difference

<222> (2)..(2)

<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc\_difference

<222> (3)..(3)

<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)

<220>

<221> misc\_difference

<222> (4)..(4)

<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)

<220>  
 <221> misc\_difference  
 <222> (5)..(6)  
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (7)..(8)  
 <223> The residues at these positions are a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (9)..(9)  
 <223> The residues at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)  
 <400> 105  
 gctcaaggca ctcttgcccta cga 23  
 <210> 106  
 <211> 8  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (1)..(1)  
 <223> The residue at this position is linked to a spacer bearing a Cy3 amidite label  
 <220>  
 <221> modified\_base  
 <222> (1)..(2)  
 <223> The residues at these positions have an amino group added.  
 <400> 106  
 ttcaccag 8

<210> 107  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (1)..(1)  
 <223> The residue at this position is a 2'deoxyctosine 5'-O-(1-Thiomon  
 ophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (2)..(2)  
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (3)..(4)  
 <223> The residues at these positions are a 2'deoxyctosine 5'-O-(1-Thi  
 omonophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (5)..(6)  
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th  
 iomonophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (7)..(7)  
 <223> The residues at these positions are a 2'deoxyctosine 5'-O-(1-Thi  
 omonophosphate)

<220>  
 <221> misc\_difference  
 <222> (8)..(8)  
 <223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Thiophosphoryl)  
 <220>  
 <221> misc\_difference  
 <222> (9)..(9)  
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiophosphoryl)  
 <400> 107  
 ctccaactac cacaagttta tattcag 27  
 <210> 108  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 108  
 cgagagacca cgct 14  
 <210> 109  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (14)..(14)  
 <223> The residue at this position contains an abasic ribose.  
 <400> 109  
 cgagagacca cgct 14

<210> 110  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (14)..(14)  
 <223> The residue at this position contains an abasic ribose with a 3' phosphate group  
 <400> 110  
 cgagagacca cgct 14  
 <210> 111  
 <211> 15  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (15)..(15)  
 <223> The residue at this position contains a 3' phosphate group.  
 <400> 111  
 cgagagacca cgctg 15  
 <210> 112  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic



<220>  
 <221> misc\_difference  
 <222> (1)..(1)  
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (2)..(2)  
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (3)..(4)  
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (5)..(5)  
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (6)..(6)  
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (7)..(8)  
 <223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (9)..(9)  
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomo  
 nophosphate)

<220>  
 <221> misc\_difference  
 <222> (10)..(10)  
 <223> The residues at these positions are a 2'deoxyctosine 5'-O-(1-Thi  
 omonophosphate)  
 <400> 112  
 gtaatcttac caacgctaac gagcgtcttg 30  
 <210> 113  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (1)..(2)  
 <223> The residues at these positions are a 2'deoxyctosine 5'-O-(1-Thi  
 omonophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (3)..(3)  
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (4)..(5)  
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th  
 iomonophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (6)..(8)  
 <223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Th  
 iomonophosphate)

<220>  
 <221> misc\_difference  
 <222> (9)..(9)  
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo  
 nophosphate)  
 <220>  
 <221> misc\_difference  
 <222> (10)..(10)  
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon  
 ophosphate)  
 <400> 113  
 cctaatttgc cagttacaaa ataaacagcc c 31  
 <210> 114  
 <211> 8  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> The residue at this position is linked to a spacer bearing a Cy3  
 dye  
 <220>  
 <221> modified\_base  
 <222> (1)..(2)  
 <223> The residues at these positions have an amino group added.  
 <400> 114  
 ttccagag 8

<210> 115  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 115  
 ttttccagag cctaataaaa ttaggctctg gaaagacgct cgtg 44  
 <210> 116  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 116  
 aacgagcgtc tttg 14  
 <210> 117  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 117  
 aacgagcgtc attg 14  
 <210> 118  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 118  
 ttttttttta attaggctct ggaaagacgc tcgtgaaacg agcgtctttg 50

<210> 119	
<211> 17	
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<220>	
<223> Synthetic	
<400> 119	
ttttccagag cctaag	17
<210> 120	
<211> 13	
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<213> Artificial Sequence	
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<223> Synthetic	
<220>	
<221> misc_difference	
<222> (1)..(1)	
<223> The residue at this position has a TET label.	
<400> 120	
ccggtcgtcc tgg	13
<210> 121	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 121	
caattccggt gtactcaccg gttcc	25
<210> 122	
<211> 16	
<212> DNA	

<213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (1)..(1)  
 <223> The residue at this position has a TET label.  
 <400> 122  
 ccggtcgtcc tggcaa 16  
 <210> 123  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 123  
 tgttttgacc tccatagaag accctatagt gagtcgtatt aatttcg 47  
 <210> 124  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 124  
 cgaaattaat acgactcact ata 23  
 <210> 125  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 125  
 cgaaattaat acgactcact ataccagaa 30

<210> 126	
<211> 16	
<212> DNA	
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<220>	
<223> Synthetic	
<400> 126	
cgaaattaat acgact	16
<210> 127	
<211> 13	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 127	
cgaaattaat acg	13
<210> 128	
<211> 12	
<212> DNA	
<213> Artificial Sequence	
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<223> Synthetic	
<400> 128	
cgaaattaat ac	12
<210> 129	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 129	
cactataggg tcttctatgg aggtc	25

<210>	130	
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<212>	DNA	
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<400>	130	
	actcactata gggctcttcta tggaggtc	28
<210>	131	
<211>	29	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	131	
	gactcactat agggctcttct atggaggtc	29
<210>	132	
<211>	30	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	132	
	cgaaattaat acgcagtatg ttagcaaacg	30
<210>	133	
<211>	30	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
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<400>	133	
	gaactggcat gattaagact ccttattacc	30



<210> 134

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 134

gaactggcat gattaagact ccttattaa

29

<210> 135

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 135

Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe  
1 5 10 15  
Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu  
20 25 30  
Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg  
35 40 45  
Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys  
50 55 60  
Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp  
65 70 75 80  
Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu  
85 90 95  
Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu  
100 105 110  
Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr  
115 120 125  
Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile  
130 135 140  
Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met  
145 150 155 160  
Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala  
165 170 175

Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys  
 180 185 190  
 Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg  
 195 200 205  
 Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp  
 210 215 220  
 Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu  
 225 230 235 240  
 Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu  
 245 250 255  
 Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp  
 260 265 270  
 Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys  
 275 280 285  
 Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His  
 290 295 300  
 Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr  
 305 310 315 320  
 Leu Asp Ala Trp Phe Lys  
 325

<210> 136

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 136

Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu  
 1 5 10 15  
 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile  
 20 25 30  
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met  
 35 40 45  
 Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg  
 50 55 60  
 Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp  
 65 70 75 80  
 Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu  
 85 90 95



<400> 137

Met	Gly	Ile	Gln	Gly	Leu	Ala	Lys	Leu	Ile	Ala	Asp	Val	Ala	Pro	Ser	1	5	10	15
Ala	Ile	Arg	Glu	Asn	Asp	Ile	Lys	Ser	Tyr	Phe	Gly	Arg	Lys	Val	Ala	20	25	30	
Ile	Asp	Ala	Ser	Met	Ser	Ile	Tyr	Gln	Phe	Leu	Ile	Ala	Val	Arg	Gln	35	40	45	
Gly	Gly	Asp	Val	Leu	Gln	Asn	Glu	Glu	Gly	Glu	Thr	Thr	Ser	His	Leu	50	55	60	
Met	Gly	Met	Phe	Tyr	Arg	Thr	Ile	Arg	Met	Met	Glu	Asn	Gly	Ile	Lys	65	70	75	80
Pro	Val	Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Gln	Leu	Lys	Ser	Gly	Glu	85	90	95	
Leu	Ala	Lys	Arg	Ser	Glu	Arg	Arg	Ala	Glu	Ala	Glu	Lys	Gln	Leu	Gln	100	105	110	
Gln	Ala	Gln	Ala	Ala	Gly	Ala	Glu	Gln	Glu	Val	Glu	Lys	Phe	Thr	Lys	115	120	125	
Arg	Leu	Val	Lys	Val	Thr	Lys	Gln	His	Asn	Asp	Glu	Cys	Lys	His	Leu	130	135	140	
Leu	Ser	Leu	Met	Gly	Ile	Pro	Tyr	Leu	Asp	Ala	Pro	Ser	Glu	Ala	Glu	145	150	155	160
Ala	Ser	Cys	Ala	Ala	Leu	Val	Lys	Ala	Gly	Lys	Val	Tyr	Ala	Ala	Ala	165	170	175	
Thr	Glu	Asp	Met	Asp	Cys	Leu	Thr	Phe	Gly	Ser	Pro	Val	Leu	Met	Arg	180	185	190	
His	Leu	Thr	Ala	Ser	Glu	Ala	Lys	Lys	Leu	Pro	Ile	Gln	Glu	Phe	His	195	200	205	
Leu	Ser	Arg	Ile	Leu	Gln	Glu	Leu	Gly	Leu	Asn	Gln	Glu	Gln	Phe	Val	210	215	220	
Asp	Leu	Cys	Ile	Leu	Leu	Gly	Ser	Asp	Tyr	Cys	Glu	Ser	Ile	Arg	Gly	225	230	235	240
Ile	Gly	Pro	Lys	Arg	Ala	Val	Asp	Leu	Ile	Gln	Lys	His	Lys	Ser	Ile	245	250	255	
Glu	Glu	Ile	Val	Arg	Arg	Leu	Asp	Pro	Asn	Lys	Tyr	Pro	Val	Pro	Glu	260	265	270	
Asn	Trp	Leu	His	Lys	Glu	Ala	His	Gln	Leu	Phe	Leu	Glu	Pro	Glu	Val	275	280	285	
Leu	Asp	Pro	Glu	Ser	Val	Glu	Leu	Lys	Trp	Ser	Glu	Pro	Asn	Glu	Glu	290	295	300	
Glu	Leu	Ile	Lys	Phe	Met	Cys	Gly	Glu	Lys	Gln	Phe	Ser	Glu	Glu	Arg	305	310	315	320



Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His Leu Ser  
 195 200 205  
 Arg Val Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val Asp Leu  
 210 215 220  
 Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly Ile Gly  
 225 230 235 240  
 Ala Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys Ser Ile Glu Glu  
 245 250 255  
 Ile Val Arg Arg Leu Asp Pro Ser Lys Tyr Pro Val Pro Glu Asn Trp  
 260 265 270  
 Leu His Lys Glu Ala Gln Gln Leu Phe Leu Glu Pro Glu Val Val Asp  
 275 280 285  
 Pro Glu Ser Val Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu Glu Leu  
 290 295 300  
 Val Lys Phe Met Cys Gly Glu Lys Gln Phe Ser Glu Glu Arg Ile Arg  
 305 310 315 320  
 Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr Gln Gly  
 325 330 335  
 Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser Ala Lys  
 340 345 350  
 Arg Lys Glu Pro Glu Pro Lys Gly Pro Ala Lys Lys Lys Ala Lys Thr  
 355 360 365  
 Gly Gly Ala Gly Lys Phe Arg Arg Gly Lys  
 370 375

<210> 139

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 139

Met Gly Ile Lys Gly Leu Asn Ala Ile Ile Ser Glu His Val Pro Ser  
 1 5 10 15  
 Ala Ile Arg Lys Ser Asp Ile Lys Ser Phe Phe Gly Arg Lys Val Ala  
 20 25 30  
 Ile Asp Ala Ser Met Ser Leu Tyr Gln Phe Leu Ile Ala Val Arg Gln  
 35 40 45  
 Gln Asp Gly Gly Gln Leu Thr Asn Glu Ala Gly Glu Thr Thr Ser His  
 50 55 60

Leu Met Gly Met Phe Tyr Arg Thr Leu Arg Met Ile Asp Asn Gly Ile  
 65 70 75 80  
 Lys Pro Cys Tyr Val Phe Asp Gly Lys Pro Pro Asp Leu Lys Ser His  
 85 90 95  
 Glu Leu Thr Lys Arg Ser Ser Arg Arg Val Glu Thr Glu Lys Lys Leu  
 100 105 110  
 Ala Glu Ala Thr Thr Glu Leu Glu Lys Met Lys Gln Glu Arg Arg Leu  
 115 120 125  
 Val Lys Val Ser Lys Glu His Asn Glu Glu Ala Gln Lys Leu Leu Gly  
 130 135 140  
 Leu Met Gly Ile Pro Tyr Ile Ile Ala Pro Thr Glu Ala Glu Ala Gln  
 145 150 155 160  
 Cys Ala Glu Leu Ala Lys Lys Gly Lys Val Tyr Ala Ala Ala Ser Glu  
 165 170 175  
 Asp Met Asp Thr Leu Cys Tyr Arg Thr Pro Phe Leu Leu Arg His Leu  
 180 185 190  
 Thr Phe Ser Glu Ala Lys Lys Glu Pro Ile His Glu Ile Asp Thr Glu  
 195 200 205  
 Leu Val Leu Arg Gly Leu Asp Leu Thr Ile Glu Gln Phe Val Asp Leu  
 210 215 220  
 Cys Ile Met Leu Gly Cys Asp Tyr Cys Glu Ser Ile Arg Gly Val Gly  
 225 230 235 240  
 Pro Val Thr Ala Leu Lys Leu Ile Lys Thr His Gly Ser Ile Glu Lys  
 245 250 255  
 Ile Val Glu Phe Ile Glu Ser Gly Glu Ser Asn Asn Thr Lys Trp Lys  
 260 265 270  
 Ile Pro Glu Asp Trp Pro Tyr Lys Gln Ala Arg Met Leu Phe Leu Asp  
 275 280 285  
 Pro Glu Val Ile Asp Gly Asn Glu Ile Asn Leu Lys Trp Ser Pro Pro  
 290 295 300  
 Lys Glu Lys Glu Leu Ile Glu Tyr Leu Cys Asp Asp Lys Lys Phe Ser  
 305 310 315 320  
 Glu Glu Arg Val Lys Ser Gly Ile Ser Arg Leu Lys Lys Gly Leu Lys  
 325 330 335  
 Ser Gly Ile Gln Gly Arg Leu Asp Gly Phe Phe Gln Val Val Pro Lys  
 340 345 350  
 Thr Lys Glu Gln Leu Ala Ala Ala Lys Arg Ala Gln Glu Asn Lys  
 355 360 365  
 Lys Leu Asn Lys Asn Lys Asn Lys Val Thr Lys Gly Arg Arg  
 370 375 380

<210> 140

<211> 387

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 140

Met	Gly	Val	His	Ser	Phe	Trp	Asp	Ile	Ala	Gly	Pro	Thr	Ala	Arg	Pro	
1				5					10					15		
Val	Arg	Leu	Glu	Ser	Leu	Glu	Asp	Lys	Arg	Met	Ala	Val	Asp	Ala	Ser	
		20						25					30			
Ile	Trp	Ile	Tyr	Gln	Phe	Leu	Lys	Ala	Val	Arg	Asp	Gln	Glu	Gly	Asn	
		35					40					45				
Ala	Val	Lys	Asn	Ser	His	Ile	Thr	Gly	Phe	Phe	Arg	Arg	Ile	Cys	Lys	
		50				55					60					
Leu	Leu	Tyr	Phe	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	Gly	Gly	Val	
65					70					75					80	
Pro	Val	Leu	Lys	Arg	Glu	Thr	Ile	Arg	Gln	Arg	Lys	Glu	Arg	Arg	Gln	
				85					90					95		
Gly	Lys	Arg	Glu	Ser	Ala	Lys	Ser	Thr	Ala	Arg	Lys	Leu	Leu	Ala	Leu	
			100					105					110			
Gln	Leu	Gln	Asn	Gly	Ser	Asn	Asp	Asn	Glu	Val	Thr	Met	Asp	Met	Ile	
		115					120					125				
Lys	Glu	Val	Gln	Glu	Leu	Leu	Ser	Arg	Phe	Gly	Ile	Pro	Tyr	Ile	Thr	
	130					135					140					
Ala	Pro	Met	Glu	Ala	Glu	Ala	Gln	Cys	Ala	Glu	Leu	Leu	Gln	Leu	Asn	
145					150					155					160	
Leu	Val	Asp	Gly	Ile	Ile	Thr	Asp	Asp	Ser	Asp	Val	Phe	Leu	Phe	Gly	
				165					170					175		
Gly	Thr	Lys	Ile	Tyr	Lys	Asn	Met	Phe	His	Glu	Lys	Asn	Tyr	Val	Glu	
			180					185					190			
Phe	Tyr	Asp	Ala	Glu	Ser	Ile	Leu	Lys	Leu	Leu	Gly	Leu	Asp	Arg	Lys	
		195					200					205				
Asn	Met	Ile	Glu	Leu	Ala	Gln	Leu	Leu	Gly	Ser	Asp	Tyr	Thr	Asn	Gly	
	210					215					220					
Leu	Lys	Gly	Met	Gly	Pro	Val	Ser	Ser	Ile	Glu	Val	Ile	Ala	Glu	Phe	
225					230					235					240	
Gly	Asn	Leu	Lys	Asn	Phe	Lys	Asp	Trp	Tyr	Asn	Asn	Gly	Gln	Phe	Asp	
				245					250					255		



Lys Arg Lys Gln Glu Thr Glu Asn Lys Phe Glu Lys Asp Leu Arg Lys  
 260 265 270  
 Lys Leu Val Asn Asn Glu Ile Ile Leu Asp Asp Asp Phe Pro Ser Val  
 275 280 285  
 Met Val Tyr Asp Ala Tyr Met Arg Pro Glu Val Asp His Asp Thr Thr  
 290 295 300  
 Pro Phe Val Trp Gly Val Pro Asp Leu Asp Met Leu Arg Ser Phe Met  
 305 310 315 320  
 Lys Thr Gln Leu Gly Trp Pro His Glu Lys Ser Asp Glu Ile Leu Ile  
 325 330 335  
 Pro Leu Ile Arg Asp Val Asn Lys Arg Lys Lys Lys Gly Lys Gln Lys  
 340 345 350  
 Arg Ile Asn Glu Phe Phe Pro Arg Glu Tyr Ile Ser Gly Asp Lys Lys  
 355 360 365  
 Leu Asn Thr Ser Lys Arg Ile Ser Thr Ala Thr Gly Lys Leu Lys Lys  
 370 375 380  
 Arg Lys Met  
 385  
 <210> 141  
 <211> 488  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 141  
 Met Gly Val Ser Gly Leu Trp Asn Ile Leu Glu Pro Val Lys Arg Pro  
 1 5 10 15  
 Val Lys Leu Glu Thr Leu Val Asn Lys Arg Leu Ala Ile Asp Ala Ser  
 20 25 30  
 Ile Trp Ile Tyr Gln Phe Leu Lys Ala Val Arg Asp Lys Glu Gly Asn  
 35 40 45  
 Gln Leu Lys Ser Ser His Val Val Gly Phe Phe Arg Arg Ile Cys Lys  
 50 55 60  
 Leu Leu Phe Phe Gly Ile Lys Pro Val Phe Val Phe Asp Gly Gly Ala  
 65 70 75 80  
 Pro Ser Leu Lys Arg Gln Thr Ile Gln Lys Arg Gln Ala Arg Arg Leu  
 85 90 95  
 Asp Arg Glu Glu Asn Ala Thr Val Thr Ala Asn Lys Leu Leu Ala Leu  
 100 105 110

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Asn Phe Leu Ala Ser Leu Thr Pro Lys Thr Asn Ser Ser Ser Ile Ser  
 450 455 460  
 Ile Glu Asn Leu Pro Arg Lys Thr Lys Leu Ser Thr Ser Leu Leu Lys  
 465 470 475 480  
 Lys Pro Ser Lys Arg Arg Arg Lys  
 485  
 <210> 142  
 <211> 550  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 142  
 Met Gly Val Gln Gly Leu Trp Lys Leu Leu Glu Cys Ser Gly Arg Gln  
 1 5 10 15  
 Val Ser Pro Glu Ala Leu Glu Gly Lys Ile Leu Ala Val Asp Ile Ser  
 20 25 30  
 Ile Trp Leu Asn Gln Ala Leu Lys Gly Val Arg Asp Arg His Gly Asn  
 35 40 45  
 Ser Ile Glu Asn Pro His Leu Leu Thr Leu Phe His Arg Leu Cys Lys  
 50 55 60  
 Leu Leu Phe Phe Arg Ile Arg Pro Ile Phe Val Phe Asp Gly Asp Ala  
 65 70 75 80  
 Pro Leu Leu Lys Lys Gln Thr Leu Val Lys Arg Arg Gln Arg Lys Asp  
 85 90 95  
 Leu Ala Ser Ser Asp Ser Arg Lys Thr Thr Glu Lys Leu Leu Lys Thr  
 100 105 110  
 Phe Leu Lys Arg Gln Ala Ile Lys Thr Glu Arg Ile Ala Ala Thr Val  
 115 120 125  
 Thr Gly Gln Met Phe Leu Glu Ser Gln Glu Leu Leu Arg Leu Phe Gly  
 130 135 140  
 Ile Pro Tyr Ile Gln Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Ile  
 145 150 155 160  
 Leu Asp Leu Thr Asp Gln Thr Ser Gly Thr Ile Thr Asp Asp Ser Asp  
 165 170 175  
 Ile Trp Leu Phe Gly Ala Arg His Val Tyr Arg Asn Phe Phe Asn Lys  
 180 185 190  
 Asn Lys Phe Val Glu Tyr Tyr Gln Tyr Val Asp Phe His Asn Gln Leu  
 195 200 205

Gly Leu Asp Arg Asn Lys Leu Ile Asn Leu Ala Tyr Leu Leu Gly Ser  
 210 215 220  
 Asp Tyr Thr Glu Gly Ile Pro Thr Val Gly Cys Val Thr Ala Met Glu  
 225 230 235 240  
 Ile Leu Asn Glu Phe Pro Gly His Gly Leu Glu Pro Leu Leu Lys Phe  
 245 250 255  
 Ser Glu Trp Trp His Glu Ala Gln Lys Asn Pro Lys Ile Arg Pro Asn  
 260 265 270  
 Pro His Asp Thr Lys Val Lys Lys Lys Leu Arg Thr Leu Gln Leu Thr  
 275 280 285  
 Pro Gly Phe Pro Asn Pro Ala Val Ala Glu Ala Tyr Leu Lys Pro Val  
 290 295 300  
 Val Asp Asp Ser Lys Gly Ser Phe Leu Trp Gly Lys Pro Asp Leu Asp  
 305 310 315 320  
 Lys Ile Arg Glu Phe Cys Gln Arg Tyr Phe Gly Trp Asn Arg Thr Lys  
 325 330 335  
 Thr Asp Glu Ser Leu Phe Pro Val Leu Lys Gln Leu Asp Ala Gln Gln  
 340 345 350  
 Thr Gln Leu Arg Ile Asp Ser Phe Phe Arg Leu Ala Gln Gln Glu Lys  
 355 360 365  
 Glu Asp Ala Lys Arg Ile Lys Ser Gln Arg Leu Asn Arg Ala Val Thr  
 370 375 380  
 Cys Met Leu Arg Lys Glu Lys Glu Ala Ala Ala Ser Glu Ile Glu Ala  
 385 390 395 400  
 Val Ser Val Ala Met Glu Lys Glu Phe Glu Leu Leu Asp Lys Ala Lys  
 405 410 415  
 Arg Lys Thr Gln Lys Arg Gly Ile Thr Asn Thr Leu Glu Glu Ser Ser  
 420 425 430  
 Ser Leu Lys Arg Lys Arg Leu Ser Asp Ser Lys Arg Lys Asn Thr Cys  
 435 440 445  
 Gly Gly Phe Leu Gly Glu Thr Cys Leu Ser Glu Ser Ser Asp Gly Ser  
 450 455 460  
 Ser Ser Glu His Ala Glu Ser Ser Ser Leu Met Asn Val Gln Arg Arg  
 465 470 475 480  
 Thr Ala Ala Lys Glu Pro Lys Thr Ser Ala Ser Asp Ser Gln Asn Ser  
 485 490 495  
 Val Lys Glu Ala Pro Val Lys Asn Gly Gly Ala Thr Thr Ser Ser Ser  
 500 505 510

Ser Asp Ser Asp Asp Asp Gly Gly Lys Glu Lys Met Val Leu Val Thr  
 515 520  
 Ala Arg Ser Val Phe Gly Lys Lys Arg Arg Lys Leu Arg Arg Ala Arg  
 530 535 540  
 Gly Arg Lys Arg Lys Thr  
 545 550  
 <210> 143  
 <211> 543  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 143  
 Met Gly Val Gln Gly Leu Trp Lys Leu Leu Glu Cys Ser Gly His Arg  
 1 5 10 15  
 Val Ser Pro Glu Ala Leu Glu Gly Lys Val Leu Ala Val Asp Ile Ser  
 20 25 30  
 Ile Trp Leu Asn Gln Ala Leu Lys Gly Val Arg Asp Ser His Gly Asn  
 35 40 45  
 Val Ile Glu Asn Ala His Leu Leu Thr Leu Phe His Arg Leu Cys Lys  
 50 55 60  
 Leu Leu Phe Phe Arg Ile Arg Pro Ile Phe Val Phe Asp Gly Asp Ala  
 65 70 75 80  
 Pro Leu Leu Lys Lys Gln Thr Leu Ala Lys Arg Arg Gln Arg Lys Asp  
 85 90 95  
 Ser Ala Ser Ile Asp Ser Arg Lys Thr Thr Glu Lys Leu Leu Lys Thr  
 100 105 110  
 Phe Leu Lys Arg Gln Ala Leu Lys Thr Asp Arg Ile Ala Ala Ser Val  
 115 120 125  
 Thr Gly Gln Met Phe Leu Glu Ser Gln Glu Leu Leu Arg Leu Phe Gly  
 130 135 140  
 Val Pro Tyr Ile Gln Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Val  
 145 150 155 160  
 Leu Asp Leu Ser Asp Gln Thr Ser Gly Thr Ile Thr Asp Asp Ser Asp  
 165 170 175  
 Ile Trp Leu Phe Gly Ala Arg His Val Tyr Lys Asn Phe Phe Asn Lys  
 180 185 190  
 Asn Lys Phe Val Glu Tyr Tyr Gln Tyr Val Asp Phe Tyr Ser Gln Leu  
 195 200 205

Gly Leu Asp Arg Asn Lys Leu Ile Asn Leu Ala Tyr Leu Leu Gly Ser  
 210 215 220  
 Asp Tyr Thr Glu Gly Ile Pro Thr Val Gly Cys Val Thr Ala Met Glu  
 225 230 235 240  
 Ile Leu Asn Glu Phe Pro Gly Arg Gly Leu Asp Pro Leu Leu Lys Phe  
 245 250 255  
 Ser Glu Trp Trp His Glu Ala Gln Asn Asn Lys Lys Val Ala Glu Asn  
 260 265 270  
 Pro Tyr Asp Thr Lys Val Lys Lys Lys Leu Arg Lys Leu Gln Leu Thr  
 275 280 285  
 Pro Gly Phe Pro Asn Pro Ala Val Ala Asp Ala Tyr Leu Arg Pro Val  
 290 295 300  
 Val Asp Asp Ser Arg Gly Ser Phe Leu Trp Gly Lys Pro Asp Val Asp  
 305 310 315 320  
 Lys Ile Arg Glu Phe Cys Gln Arg Tyr Phe Gly Trp Asn Arg Met Lys  
 325 330 335  
 Thr Asp Glu Ser Leu Tyr Pro Val Leu Lys His Leu Asn Ala His Gln  
 340 345 350  
 Thr Gln Leu Arg Ile Asp Ser Phe Phe Arg Leu Ala Gln Gln Glu Lys  
 355 360 365  
 Gln Asp Ala Lys Leu Ile Lys Ser His Arg Leu Ser Arg Ala Val Thr  
 370 375 380  
 Cys Met Leu Arg Lys Glu Arg Glu Glu Lys Ala Pro Glu Leu Thr Lys  
 385 390 395 400  
 Val Thr Glu Ala Met Glu Lys Glu Phe Glu Leu Leu Asp Asp Ala Lys  
 405 410 415  
 Gly Lys Thr Gln Lys Arg Glu Leu Pro Tyr Lys Lys Glu Thr Ser Val  
 420 425 430  
 Pro Lys Arg Arg Arg Pro Ser Gly Asn Gly Gly Phe Leu Gly Asp Pro  
 435 440 445  
 Tyr Cys Ser Glu Ser Pro Gln Glu Ser Ser Cys Glu Asp Gly Glu Gly  
 450 455 460  
 Ser Ser Val Met Ser Ala Arg Gln Arg Ser Ala Ala Glu Ser Ser Lys  
 465 470 475 480  
 Ile Gly Cys Ser Asp Val Pro Asp Leu Val Arg Asp Ser Pro His Gly  
 485 490 495  
 Arg Gln Gly Cys Val Ser Thr Ser Ser Ser Asp Ser Glu Asp Gly Glu  
 500 505 510  
 Asp Lys Ala Lys Thr Val Leu Val Thr Ala Arg Pro Val Phe Gly Lys  
 515 520 525  
 Lys Arg Arg Lys Leu Lys Ser Met Lys Arg Arg Lys Lys Lys Thr  
 530 535 540

<210> 144

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 144

Met Gly Val Gln Gly Leu Trp Lys Leu Leu Glu Cys Ser Gly Arg Pro  
1 5 10 15  
Ile Asn Pro Gly Thr Leu Glu Gly Lys Ile Leu Ala Val Asp Ile Ser  
20 25 30  
Ile Trp Leu Asn Gln Ala Val Lys Gly Ala Arg Asp Arg Gln Gly Asn  
35 40 45  
Ala Ile Gln Asn Ala His Leu Leu Thr Leu Phe His Arg Leu Cys Lys  
50 55 60  
Leu Leu Phe Phe Arg Ile Arg Pro Ile Phe Val Phe Asp Gly Glu Ala  
65 70 75 80  
Pro Leu Leu Lys Arg Gln Thr Leu Ala Lys Arg Arg Gln Arg Thr Asp  
85 90 95  
Lys Ala Ser Asn Asp Ala Arg Lys Thr Asn Glu Lys Leu Leu Arg Thr  
100 105 110  
Phe Leu Lys Arg Gln Ala Ile Lys Ala Glu Arg Ile Ala Ala Thr Val  
115 120 125  
Thr Gly Gln Met Cys Leu Glu Ser Gln Glu Leu Leu Gln Leu Phe Gly  
130 135 140  
Ile Pro Tyr Ile Val Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Ile  
145 150 155 160  
Leu Asp Leu Thr Asp Gln Thr Ser Gly Thr Ile Thr Asp Asp Ser Asp  
165 170 175  
Ile Trp Leu Phe Gly Ala Arg His Val Tyr Lys Asn Phe Phe Ser Gln  
180 185 190  
Asn Lys His Val Glu Tyr Tyr Gln Tyr Ala Asp Ile His Asn Gln Leu  
195 200 205  
Gly Leu Asp Arg Ser Lys Leu Ile Asn Leu Ala Tyr Leu Leu Gly Ser  
210 215 220  
Asp Tyr Thr Glu Gly Ile Pro Thr Val Gly Tyr Val Ser Ala Met Glu  
225 230 235 240  
Ile Leu Asn Glu Phe Pro Gly Gln Gly Leu Glu Pro Leu Val Lys Phe  
245 250 255

Lys Glu Trp Trp Ser Glu Ala Gln Lys Asp Lys Lys Met Arg Pro Asn  
 260 265 270  
 Pro Asn Asp Thr Lys Val Lys Lys Lys Leu Arg Leu Leu Asp Leu Gln  
 275 280 285  
 Gln Ser Phe Pro Asn Pro Ala Val Ala Ser Ala Tyr Leu Lys Pro Val  
 290 295 300  
 Val Asp Glu Ser Lys Ser Ala Phe Ser Trp Gly Arg Pro Asp Leu Glu  
 305 310 315 320  
 Gln Ile Arg Glu Phe Cys Glu Ser Arg Phe Gly Trp Tyr Arg Leu Lys  
 325 330 335  
 Thr Asp Glu Val Leu Leu Pro Val Leu Lys Gln Leu Asn Ala Gln Gln  
 340 345 350  
 Thr Gln Leu Arg Ile Asp Ser Phe Phe Arg Leu Glu Gln His Glu Ala  
 355 360 365  
 Ala Gly Leu Lys Ser Gln Arg Leu Arg Arg Ala Val Thr Cys Met Lys  
 370 375 380  
 Arg Lys Glu Arg Asp Val Glu Ala Glu Glu Val Glu Ala Ala Val Ala  
 385 390 395 400  
 Val Met Glu Arg Glu Cys Thr Asn Gln Arg Lys Gly Gln Lys Thr Asn  
 405 410 415  
 Thr Lys Ser Gln Gly Thr Lys Arg Arg Lys Pro Thr Glu Cys Ser Gln  
 420 425 430  
 Glu Asp Gln Asp Pro Gly Gly Gly Phe Ile Gly Ile Glu Leu Lys Thr  
 435 440 445  
 Leu Ser Ser Lys Ala Tyr Ser Ser Asp Gly Ser Ser Ser Asp Ala Glu  
 450 455 460  
 Asp Leu Pro Ser Gly Leu Ile Asp Lys Gln Ser Gln Ser Gly Ile Val  
 465 470 475 480  
 Gly Arg Gln Lys Ala Ser Asn Lys Val Glu Ser Ser Ser Ser Ser Asp  
 485 490 495  
 Asp Glu Asp Arg Thr Val Met Val Thr Ala Lys Pro Val Phe Gln Gly  
 500 505 510  
 Lys Lys Thr Lys Ser Lys Thr Met Lys Glu Thr Val Lys Arg Lys  
 515 520 525  
 <210> 145  
 <211> 434  
 <212> PRT



<213> Artificial Sequence

<220>

<223> Synthetic

<400> 145

Met Thr Ile Asn Gly Ile Trp Glu Trp Ala Asn His Val Val Arg Lys  
1 5 10 15  
Val Pro Asn Glu Thr Met Arg Asp Lys Thr Leu Ser Ile Asp Gly His  
20 25 30  
Ile Trp Leu Tyr Glu Ser Leu Lys Gly Cys Glu Ala His His Gln Gln  
35 40 45  
Thr Pro Asn Ser Tyr Leu Val Thr Phe Phe Thr Arg Ile Gln Arg Leu  
50 55 60  
Leu Glu Leu Lys Ile Ile Pro Ile Val Val Phe Asp Asn Ile Asn Ala  
65 70 75 80  
Ser Ser Ser Ala His Glu Ser Lys Asp Gln Asn Glu Phe Val Pro Arg  
85 90 95  
Lys Arg Arg Ser Phe Gly Asp Ser Pro Phe Thr Asn Leu Val Asp His  
100 105 110  
Val Tyr Lys Thr Asn Ala Leu Leu Thr Glu Leu Gly Ile Lys Val Ile  
115 120 125  
Ile Ala Pro Gly Asp Gly Glu Ala Gln Cys Ala Arg Leu Glu Asp Leu  
130 135 140  
Gly Val Thr Ser Gly Cys Ile Thr Thr Asp Phe Asp Tyr Phe Leu Phe  
145 150 155 160  
Gly Gly Lys Asn Leu Tyr Arg Phe Asp Phe Thr Ala Gly Thr Ser Ser  
165 170 175  
Thr Ala Cys Leu His Asp Ile Met His Leu Ser Leu Gly Arg Met Phe  
180 185 190  
Met Glu Lys Lys Val Ser Arg Pro His Leu Ile Ser Thr Ala Ile Leu  
195 200 205  
Leu Gly Cys Asp Tyr Phe Gln Arg Gly Val Gln Asn Ile Gly Ile Val  
210 215 220  
Ser Val Phe Asp Ile Leu Gly Glu Phe Gly Asp Asp Gly Asn Glu Glu  
225 230 235 240  
Ile Asp Pro His Val Ile Leu Asp Arg Phe Ala Ser Tyr Val Arg Glu  
245 250 255  
Glu Ile Pro Ala Arg Ser Glu Asp Thr Gln Arg Lys Leu Arg Leu Arg  
260 265 270  
Arg Lys Lys Tyr Asn Phe Pro Val Gly Phe Pro Asn Cys Asp Ala Val  
275 280 285

His Asn Ala Ile Thr Met Tyr Leu Arg Pro Pro Val Ser Ser Glu Ile  
 290 295 300  
 Pro Lys Ile Ile Pro Arg Ala Ala Asn Phe Gln Gln Val Ala Glu Ile  
 305 310 315 320  
 Met Met Lys Glu Cys Gly Trp Pro Ala Thr Arg Thr Gln Lys Glu Leu  
 325 330 335  
 Ala Leu Ser Ile Arg Arg Lys Val His Leu Thr Thr Thr Val Ala Gln  
 340 345 350  
 Thr Arg Ile Pro Asp Phe Phe Ala Ala Thr Lys Ser Lys Asn Phe Thr  
 355 360 365  
 Pro Ile Val Glu Pro Cys Glu Ser Leu Glu Asp Tyr Ile Ser Ala Asn  
 370 375 380  
 Asn Thr Trp Met Arg Lys Arg Lys Arg Ser Glu Ser Pro Gln Ile Leu  
 385 390 395 400  
 Gln His His Ala Lys Arg Gln Val Pro Asp Arg Lys Arg Ser Val Lys  
 405 410 415  
 Ile Arg Ala Phe Lys Pro Tyr Pro Thr Asp Val Ile Glu Leu Gly Asp  
 420 425 430  
 Ser Asp

<210> 146

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 146

tactgactca ctatagggtc ttctatggag gtc

33

<210> 147

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 147	
ttttttttta attaggctct ggaagacgct gaaagcgtct tg	42
<210> 148	
<211> 38	
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<213> Artificial Sequence	
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<400> 148	
ttttttttta attaggctct ggaagacgga acgtcttg	38
<210> 149	
<211> 34	
<212> DNA	
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<400> 149	
ttttttttta attaggctct ggaagagaat cttg	34
<210> 150	
<211> 32	
<212> DNA	
<213> Artificial Sequence	
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<400> 150	
ttttttttta attaggctct ggaaggaact tg	32
<210> 151	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
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<400> 151	
tttttttttta attaggctct ggaag	25
<210> 152	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<220>	
<221> misc_difference	
<222> (1)..(1)	
<223> The residue at this position has a TET label.	
<400> 152	
attagaaagg aagggaagaa agcgaa	26
<210> 153	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 153	
acggggaaag ccggcgaacg tggcgagaaa	30
<210> 154	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 154	
tgacggggaa agccggcgaa cgtggcgaga	30

<210> 155  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 155  
 cttgacgggg aaagccggcg aacgtggcga 30  
 <210> 156  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 156  
 gcttgacggg gaaagccggc gaacgtggcg 30  
 <210> 157  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> The residue at this position contains a fluorescein label.  
 <400> 157  
 agaaaggaag ggaagaaa 18  
 <210> 158  
 <211> 45  
 <212> DNA

<213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (1)..(1)  
 <223> The residue at this position contains a fluorescein label.  
 <400> 158  
 tggaggtcaa aacatcgata agtcgaagaa aggaagggaa gaaat 45  
 <210> 159  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (1)..(1)  
 <223> The residue at this position contains a fluorescein label.  
 <400> 159  
 tgttttgacc tcca 14  
 <210> 160  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 160  
 acacagtgtc ctcccgtcc tcctgagcaa 30  
 <210> 161  
 <211> 18  
 <212> DNA

<213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (1)..(1)  
 <223> The residue at this position contains a fluorescein label.  
 <400> 161  
 tttccctcct cctcttcc 18  
 <210> 162  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 162  
 atgaggaaga ggaggagggt gtcaggagg agcgggagga cactgtgtct gtca 54  
 <210> 163  
 <211> 53  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 163  
 ttcgctttct tcccttcctt tctcgccacg ttcgccggt ttccccgtca agc 53  
 <210> 164  
 <211> 1011  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic

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<400> 164
atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60
ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180
atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtggt tgtattcgac 240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag 300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360
caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct ttaagtac 420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc 540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaatgtc 600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg 660
acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg 720
aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg 780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg 840
aatcctcctg tgactgacga ctacagaata gaggtcaggg agcctgactt tgagaaggcc 900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag 960
aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtggttctg a 1011

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<210> 165

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 165

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Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1           5           10           15
Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
20           25           30
Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35           40           45
Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50           55           60

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Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	65	70	75	80
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys	85	90	95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly	100	105	110	
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu	115	120	125	
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro	130	135	140	
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala	145	150	155	160
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu	165	170	175	
Leu	Phe	Gly	Ser	Pro	Arg	Leu	Ala	Arg	Asn	Leu	Ala	Ile	Thr	Gly	Lys	180	185	190	
Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Asp	Val	Lys	Pro	Glu	Ile	195	200	205	
Ile	Ile	Leu	Glu	Ser	Asn	Leu	Lys	Arg	Leu	Gly	Leu	Thr	Arg	Glu	Gln	210	215	220	
Leu	Ile	Asp	Ile	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Glu	Gly	Val	225	230	235	240
Lys	Gly	Val	Gly	Val	Lys	Lys	Ala	Leu	Asn	Tyr	Ile	Lys	Thr	Tyr	Gly	245	250	255	
Asp	Ile	Phe	Arg	Ala	Leu	Lys	Ala	Leu	Lys	Val	Asn	Ile	Asp	His	Val	260	265	270	
Glu	Glu	Ile	Arg	Asn	Phe	Phe	Leu	Asn	Pro	Pro	Val	Thr	Asp	Asp	Tyr	275	280	285	
Arg	Ile	Glu	Phe	Arg	Glu	Pro	Asp	Phe	Glu	Lys	Ala	Ile	Glu	Phe	Leu	290	295	300	
Cys	Glu	Glu	His	Asp	Phe	Ser	Arg	Glu	Arg	Val	Glu	Lys	Ala	Leu	Glu	305	310	315	320
Lys	Leu	Lys	Ala	Leu	Lys	Ser	Thr	Gln	Ala	Thr	Leu	Glu	Arg	Trp	Phe	325	330	335	

<210> 166

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 166 ccgtcaacat ttaccatggg tgcgga	26
<210> 167	
<211> 31	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 167 ccgccacctc gtagtcgaca tccttttcgt g	31
<210> 168	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 168 ggcgaccaca cccgtcctgt	20
<210> 169	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 169 ccacgatgcg tccggcgtag	20
<210> 170	
<211> 29	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	

<220>  
 <221> modified\_base  
 <222> (29)..(29)  
 <223> The residue at this position is a 3' amine.  
 <400> 170  
 aacgaggcgc acccacccaa ggcacagcn 29  
 <210> 171  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 171  
 acgggtcaat gtccatgccc caaaga 26  
 <210> 172  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (23)..(27)  
 <223> The residues at these positions are 2'-O-methyls.  
 <220>  
 <221> modified\_base  
 <222> (28)..(28)  
 <223> The residue at this position is a 3' amine.  
 <400> 172  
 gtctgagatg aaagtgcgcc tcgttaan 28

<210> 173  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 173  
 tcttcgcaca ttcatctca gacgga 26  
 <210> 174  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (1)..(21)  
 <223> The residues at these positions are 2'-O-methyls.  
 <220>  
 <221> modified\_base  
 <222> (22)..(22)  
 <223> The residue at this position is a 3' amine.  
 <400> 174  
 gctgtgcctt ggggtgggtgc gn 22  
 <210> 175  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>

<221> modified\_base  
 <222> (29)..(29)  
 <223> The residue at this position is a 3' amine.  
 <400> 175  
 aacgaggcgc acccacccaa ggcacagcn 29  
 <210> 176  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 176  
 acgggtcaat gtccatgccc caaaga 26  
 <210> 177  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (23)..(27)  
 <223> The residues at these positions are 2'-O-methyls.  
 <220>  
 <221> modified\_base  
 <222> (28)..(28)  
 <223> The residue at this position is a 3' amine.  
 <400> 177  
 gtctgagatg aaagtgcgcc tcgttaan 28

<210> 178  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> The residue at this position is linked to a spacer containing a f  
 luorescein label  
  
 <400> 178  
 tcttcgcaca ttcatctca gac 23  
  
 <210> 179  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (1)..(17)  
 <223> The residues at these positions are 2'-O-methyls.  
 <220>  
 <221> modified\_base  
 <222> (18)..(18)  
 <223> The residue at this position is a 3' amine.  
  
 <400> 179  
 gctgtgcctt gggtgggn 18

<210> 180  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (1)..(19)  
 <223> The residues at these positions are 2'-O-methyls.  
 <220>  
 <221> modified\_base  
 <222> (20)..(20)  
 <223> The residue at this position is a 3' amine.

<400> 180  
 gctgtgcctt ggggtgggtgn

20

<210> 181  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (1)..(21)  
 <223> The residues at these positions are 2'-O-methyls.  
 <220>  
 <221> modified\_base  
 <222> (22)..(22)  
 <223> The residue at this position is a 3' amine.

<400> 181  
 gctgtgcctt ggggtgggtgc gn

22

<210> 182  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (1)..(22)  
 <223> The residues at these positions are 2'-O-methyls.  
 <220>  
 <221> modified\_base  
 <222> (23)..(23)  
 <223> The residue at this position is a 3' amine.  
 <400> 182  
 gctgtgcctt ggggtgggtgc gcn

23

<210> 183  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> The residue at this position is linked to a spacer containing a f  
 luorescein label  
 <220>  
 <221> modified\_base  
 <222> (22)..(22)  
 <223> The residue at this position indicates 2'-O-methyl sugar.



<220>  
 <221> modified\_base  
 <222> (42)..(42)  
 <223> The residue at this position is a 3' amine.  
 <400> 183  
 gtctgagatg aaagtgctcc cgcacccacc caaggcacag cn 42  
 <210> 184  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (1)..(17)  
 <223> The residues at these positions are 2'-O-methyl sugars.  
 <220>  
 <221> modified\_base  
 <222> (18)..(18)  
 <223> The residue at this position is a 3' amine.  
 <400> 184  
 gctgtgcctt gggtgggn 18  
 <210> 185  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_difference  
 <222> (29)..(29)  
 <223> The residue at this position is a 3' primer.

<400> 185  
 aacgaggcgc acccacccaa ggcacagcn 29  
 <210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 186  
 gctgtgcctt ggggtgggtgc g 21  
 <210> 187  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (21)..(21)  
 <223> The residue at this position is a 3' amine.  
 <400> 187  
 gctgtgcctt ggggtgggtgc n 21  
 <210> 188  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (15)..(20)  
 <223> The residues at these positions are 2'-O-methyl sugars.

<220>  
 <221> modified\_base  
 <222> (21)..(21)  
 <223> The residue at this position is a 3' amine.  
 <400> 188  
 gctgtgcctt ggggtgggtgc n 21  
 <210> 189  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> modified\_base  
 <222> (1)..(20)  
 <223> The residues at these positions are 2'-O-methyl sugars.  
 <220>  
 <221> modified\_base  
 <222> (21)..(21)  
 <223> The residue at this position is a 3' amine.  
 <400> 189  
 gctgtgcctt ggggtgggtgc n 21  
 <210> 190  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic

<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> The residue at this position is linked to a spacer containing a f  
 luorescein label  
 <400> 190  
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 <210> 191  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 191  
 ctgggcgcgg acatggagga cgtgcgcggc cgcctggtgc agtaccgcgg cgag 54  
 <210> 192  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 192  
 ctgggcgcgg acatggagga cgtgtgcggc cgcctggtgc agtaccgcgg cgag 54  
 <210> 193  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence  
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 <400> 193  
 cgcgatgccg atgacctgca gaagcgctg gcagtgtacc aggccggggc ccgcga 56

<210> 194  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence  
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 <400> 194  
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 <210> 195  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> cggtactgcaccaggcggccgct  
 <400> 195  
 cggtactgca ccaggcggcc gct 23  
 <210> 196  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
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 ccccggcctg gtacactgcc aggct 25  
 <210> 197  
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 <223> Synthetic  
 <400> 197  
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 <222> (24)..(24)  
 <223> The residue at this position is linked to 2-amino deoxyadenosine.  
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 <221> misc\_feature  
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 <223> The residue at this position is linked to 2-amino deoxyadenosine.  
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<210> 201  
 <211> 39  
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 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye  
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 <211> 28  
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 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 203  
 gggctccaca cggcgactct catt 24

<210> 204  
 <211> 39  
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 <400> 204  
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 <210> 205  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
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 ggtgctccac ctggtacgta tatctctgct cttccccag 39  
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 <211> 46  
 <212> DNA  
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 <220>  
 <223> Synthetic  
 <400> 206  
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 <210> 207  
 <211> 46  
 <212> DNA  
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 <223> Synthetic  
 <400> 207  
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 <212> DNA  
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 <400> 208  
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 <211> 27  
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 <213> Artificial Sequence  
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 <211> 40  
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 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> The residue at this position is linked to a spacer bearing a Cy3  
 dye  
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 <210> 211  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic  
 <400> 211  
 aagcacgcag cacgatcata gaacacgaac agttt 35  
 <210> 212  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 212  
 aagcacgcag caccatcata gaacacgaac agttt 35  
 <210> 213  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 213  
 acgcgtctcg gttttccgag acgcgtgtgc tgcgtgcuuu 40  
 <210> 214  
 <211> 50  
 <212> DNA  
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 <220>  
 <223> Synthetic  
 <400> 214  
 gaagggtgtct gcgggagccg atttcatcat cacgcagctt ttctttgagg 50

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	caaagaaaag ctgcgtgatg atgaaatcgc	30
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<212>	DNA	
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<400>	217	
	aacgaggcgc acgctcccgc agacac	26
<210>	218	
<211>	27	
<212>	DNA	
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<400>	218	
	aacgaggcgc acactcccgc agacacc	27

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 <212> DNA  
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 <221> misc\_feature  
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 <223> The residue at this position is linked to a spacer bearing a Cy3 dye  
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 <210> 220  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
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 <400> 220  
 actgggagca ttgaggctcg ctgagagtca cttttattgg gaaccatagt t 51  
 <210> 221  
 <211> 51  
 <212> DNA  
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 <400> 221  
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 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 222  
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 <210> 223  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 223  
 aacgaggcgc acgagcctca atgctccc 28  
 <210> 224  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
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 aacgaggcgc acaagcctca atgctccc 28  
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 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic

<220>  
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 <223> The residue at this position is a spacer bearing a Cy3 dye.  
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 <210> 226  
 <211> 52  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 226  
 tgaagtctag agaaagggtt gtacggctga ggtctggaga aatgggcata tg 52  
 <210> 227  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 227  
 tttgaaatgt cacagggttc ctaacagcca ctcttccttg gatggg 46  
 <210> 228  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 228  
 agatgcccac ttctccagac ctcagccc 28

<210> 229  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
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 aagcacgcag cacgtacaac cctttctcta gacaaa 36  
 <210> 230  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> The residue at this position is linked to a spacer bearing a Cy3  
 dye  
 <400> 230  
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 <210> 231  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
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 <400> 231  
 ccatccaggg aagagtggcc tgttt 25

<210> 232  
 <211> 29  
 <212> DNA  
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 <223> Synthetic  
 <400> 232  
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 <210> 233  
 <211> 46  
 <212> DNA  
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 <400> 233  
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 <210> 234  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence  
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 <210> 235  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 235  
 gaccctggag gctgaacccc gtcca 25



<210> 236  
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 <212> DNA  
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 <223> Synthetic  
 <400> 236  
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 <210> 237  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 237  
 aacgaggcgc actcatgccc ctcaaaac 28  
 <210> 238  
 <211> 56  
 <212> DNA  
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 aaggacaaaa tacctgtatt cctcgctgt ccagggatct gctcttacag attaga 56  
 <210> 239  
 <211> 56  
 <212> DNA  
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 aaggacaaaa tacctgtatt ccttgctgt ccagggatct gctcttacag attaga 56

<210> 240  
 <211> 30  
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 <223> Synthetic  
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 <221> misc\_feature  
 <222> (28)..(28)  
 <223> The residue at this position is linked to a purine.  
 <400> 240  
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 <210> 241  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
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 aacgaggcgc acgaggaata caggtatttt gtc 33  
 <210> 242  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
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 <400> 242  
 aacgaggcgc acaaggaata caggtatttt gtc 33

<210> 243  
 <211> 24  
 <212> DNA  
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 <400> 243  
 ggtaaagggtt ggcaaaaaga taac 24  
 <210> 244  
 <211> 27  
 <212> DNA  
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 <223> Synthetic  
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 <223> Synthetic  
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 <221> misc\_feature  
 <222> (4)..(4)  
 <223> The residue at this position is linked to a spacer bearing a Cy3  
 dye  
 <400> 245  
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 <210> 246  
 <211> 29  
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<220>  
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 <210> 247  
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 cgcgccgagg acaccttttt tagggtgctt tgt 33  
 <210> 248  
 <211> 22  
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 aaaatcgatg gtaaagggttg gc 22  
 <210> 249  
 <211> 22  
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 <400> 249  
 agttctgcag taccggattt gc 22

<210> 250  
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 <211> 20  
 <212> DNA  
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 <400> 251  
 gtaaacataa gcaactttag 20  
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 <211> 41  
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 <210> 253  
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